SEQUENCE LISTING

5	(1) GENE	RAL INFORMATION:
J	(i)	APPLICANT: Glimcher, Laurie H. et al.
10	(ii)	TITLE OF INVENTION: Human c-Maf Compositions and Methods of Use Thereof
10	(iii)	NUMBER OF SEQUENCES: 2
15	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP (B) STREET: 28 State Street (C) CITY: Boston (D) STATE: Massachusetts (E) COUNTRY: USA (F) ZIP: 02109
20	(v)	COMPUTER READABLE FORM:
25	,,,	 (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
30	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
35	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 09/030,579 (B) FILING DATE: 2-FEB-1998
	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Kara, Catherine J. (B) REGISTRATION NUMBER: 41,106
40		(C) REFERENCE/DOCKET NUMBER: HUI-027CP
	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (617)227-7400 (B) TELEFAX: (617)742-4214
45		
	(2) INFO	RMATION FOR SEQ ID NO:1:
50	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 1203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
55	(ii)	MOLECULE TYPE: cDNA
	(ix)	FEATURE:

AND STATE OF THE PARTY OF THE PARTY.

(A) NAME/KEY: CDS

(B) LOCATION: 1..1203

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:															
	ATG	GCA	TCA	GAA	CTG	GCA	ATG	AGC	AAC	TCC	GAC	CTG	CCC	ACC	AGT	CCC
10		Ala	Ser	Glu	Leu 5	Ala	Met	Ser	Asn	Ser 10	Asp	Leu	Pro	Thr	Ser 15	Pro
	CTG 96	GCC	ATG	GAA	TAT	GTT	AAT	GAC	TTC	GAT	CTG	ATG	AAG	TTT	GAA	GTG
15	Leu	Ala	Met	Glu 20	Tyr	Val	Asn	Asp	Phe 25	Asp	Leu	Met	Lys	Phe 30	Glu	Val
	AAA 144	AAG	GAA	CCG	GTG	GAG	ACC	GAC	CGC	ATC	ATC	AGC	CAG	TGC	GGC	CGT
20	Lys	Lys	Glu 35	Pro	Val	Glu	Thr	Asp 40	Arg	Ile	Ile	Ser	Gln 45	Cys	Gly	Arg
	CTC 192	ATC	GCC	GGG	GGC	TCG	CTG	TCC	TCC	ACC	CCC	ATG	AGC	ACG	CCC	TGC
25		Ile 50	Ala	Gly	Gly	Ser	Leu 55	Ser	Ser	Thr	Pro	Met 60	Ser	Thr	Pro	Cys
	AGC 240	TCG	GTG	CCC	CCG	TCC	CCC	AGC	TTC	TCG	GCG	CCC	AGC	CCG	GGC	TCG
30	Ser 65	Ser	Val	Pro	Pro	Ser 70	Pro	Ser	Phe	Ser	Ala 75	Pro	Ser	Pro	Gly	Ser 80
	CGA 288	GGC	GAA	CAG	AAG	GCG	CAC	CTG	GAA	GAC	TAC	TAC	TGG	ATG	ACC	GGC
35		Gly	Glu	Gln	Lys 85	Ala	His	Leu	Glu	Asp 90	Tyr	Tyr	Trp	Met	Thr 95	Gly
	TAC	CCG	CAG	CAG	CTG	AAC	CCC	GAG	GCG	CTG	GGC	TTC	AGC	CCC	GAG	GAC
40		Pro	Gln	Gln 100	Leu	Asn	Pro	Glu	Ala 105	Leu	Gly	Phe	Ser	Pro 110	Glu	Asp
	GCG 384	GTC	GAG	GCG	CTC	ATC	AGC	AAC	AGC	CAC	CAG	CTC	CGG	GGC	GGC	TTC
45	Ala	Val	Glu 115	Ala	Leu	Ile	Ser	Asn 120	Ser	His	Gln	Leu	Arg 125	Gly	Gly	Phe
	GAT 432	GGC	TAT	GCG	CGC	GGG	GCG	CAG	CAG	CTA	GCC	GCG	GCG	GCC	GGG	GCA
50	Asp	Gly 130	Tyr	Ala	Arg	Gly	Ala 135	Gln	Gln	Leu	Ala	Ala 14∪	Ala	Ala	Gly	Ala
	GGT 480	GCC	GGC	GCC	TCC	TTG	GGC	GGC	AGC	GGC	GAG	GAG	ATG	GGC	CCC	GCC
55		Ala	Gly	Ala	Ser	Leu 150	Gly	Gly	Ser	Gly	Glu 155	Glu	Met	Gly	Pro	Ala 160

	GCC 528	GCC	GTG	GTG	TCC	GCC	GTG	ATC	GCC	GCG	GCC	GCC	GCG	CAG	AGC	GGC
5	Ala	Ala	Val	Val	Ser 165	Ala	Val	Ile	Ala	Ala 170	Ala	Ala	Ala	Gln	Ser 175	Gly
J	GCG 576	GGC	CCG	CAC	TAC	CAC	CAC	CAC	CAC	CAC	CAC	GCC	GCC	GGC	CAC	CAC
10	Ala	Gly	Pro	His 180	Tyr	His	His	His	His 185	His	His	Ala	Ala	Gly 190	His	His
10	CAC 624	CAC	CCG	ACG	GCC	GGC	GCG	CCC	GGC	GCC	GCG	GGC	AGC	GCG	GCC	GCT
15	His	His	Pro 195	Thr	Ala	Gly	Ala	Pro 200	Gly	Ala	Ala	Gly	Ser 205	Ala	Ala	Ala
13	TCG 672	GCC	GGT	GGC	GCT	GGG	GGC	GCG	GGC	GGC	GGT	GGC	CCG	GCC	AGC	GTT
20	Ser	Ala 210	Gly	Gly	Ala	Gly	Gly 215	Ala	Gly	Gly	Gly	Gly 220	Pro	Ala	Ser	Val
20	GGG 720	GGC	GGA	GGC	GGC	GGG	GGC	GCG	GCG							
25	Gly 225	Gly	Gly	Gly	Gly	Gly 230	Gly	Gly	Gly	Gly	Gly 235	Gly	Gly	Gly	Ala	Ala 240
23	GGC 768	GCC	CTG	CAC	CCG	CAC	CAC	GCC	GCC	GGC	GGC	CTG	CAC	TTC	GAC	GAC
30	Gly	Ala	Leu	His	Pro 245	His	His	Ala	Ala	Gly 250	Gly	Leu	His	Phe	Asp 255	Asp
30	CGC 816	TTC	TCC	GAC	GAG	CAG	CTG	GTG	ACC	ATG	TCT	GTG	CGC	GAC	TGG	AAC
35	Arg	Phe	Ser	Asp 260	Glu	Gln	Leu	Val	Thr 265	Met	Ser	Val	Arg	Asp 270	Trp	Asn
33	CGG 864	CAG	CTG	CGC	GGG	GTC	AGC	AAG	GAG	GAG	GTG	ATC	CGG	CTG	AAG	CAG
40	Arg	Gln	Leu 275	Arg	Gly	Val	Ser	Lys 280	Glu	Glu	Val	Ile	Arg 285	Leu	Lys	Gln
40	AAG 912	AGG	CGG	ACC	CTG	AAA	AAC	CGC	GGC	TAT	GCC	AAG	TCC	TGC	CGC	TTC
45	Lys	Arg 290	Arg	Thr	Leu	Lys	Asn 295	Arg	Gly	Tyr	Ala	Lys 300	Ser	Cys	Arg	Phe
43	AAG 960	AGG	GTG	CAG	CAG	AGA	CAC	GTC	CTG	GAG	TCG	GAG	AAG	AAC	CAG	CTG
50	Lys 305	Arg	Val	Gln	Gln	Arg 310	His	Val	Leu	Glu	Ser 315	Glu	Lys	Asn	Gln	Leu 320
50	CTG		CAA	GTC	GAC	CAC	CTC	AAG	CAG	GAG	ATC	TCC	AGG	CTG	GTG	CGC
55			Gln	Val	Asp 325	His	Leu	Lys	Gln	Glu 330	Ile	Ser	Arg	Leu	Val 335	Arg
55	GAG 105		GAC	GCG	TAC	AAG	GAG	AAA	TAC	GAG	AAG	TTG	GTG	AGC	AGC	GGC

	Glu i	Arg	Asp	Ala 340	Tyr	Lys	Glu	Lys	Tyr 345	Glu	Lys	Leu	Val	Ser 350	Ser (Gly
_	TTC	CGA	GAA	AAC	GGC	TCG	AGC	AGC	GAC	AAC	CCG	TCC	TCT	CCC	GAG	TTT
5	1104 Phe	Arg	Glu 355	Asn	Gly	Ser	Ser	Ser 360	Asp	Asn	Pro	Ser	Ser 365	Pro	Glu	Phe
10	TTC	ATA	ACT	GAG	CCC	ACT	CGC	AAG	TTG	GAG	CCA	TCA	GTG	GGA	TAC	GCC
10		Ile 370	Thr	Glu	Pro	Thr	Arg 375	Lys	Leu	Glu	Pro	Ser 380	Val	Gly	Tyr	Ala
15	ACA 1200		TGG	AAG	CCC	CAG	CAT	CGT	GTA	CTT	ACC	AGT	GTG	TTC	ACA	AAA
15	Thr 385	Phe	Trp	Lys	Pro	Gln 390	His	Arg	Val	Leu	Thr 395	Ser	Val	Phe	Thr	Lys 400
20	TGA 1203															
25																
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein															
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:															
35	Met 1	Ala	Ser	Glu	Leu 5		Met	Ser	Asn	Ser 10	Asp	Leu	Pro	Thr	Ser 15	Pro
40	Leu	Ala	Met	Glu 20		Val	Asn	Asp	Phe 25		Leu	Met	Lys	Phe 30	Glu	Val
	Lys	Lys	Glu 35		Val	. Glu	Thr	Asp 40		, Ile	lle	Ser	Gln 45		Gly	Arg
45	Leu	Ile 50		ı Gly	√ Gly	ser Ser	Leu 55		Ser	Thr	Pro	Met 60		Thr	Pro	Cys
5.`	Ser 65		Val	L Pro	Pro	Ser 70		Ser	Phe	e Sei	r Ala 75		Se1	r Pro	Gly	Ser 80
J.	Arg	Gl	/ Gli	ı Glr	n Lys 85		a His	: Lei	ı Glı	u Asp 90		туг	Tr	o Met	: Thr 95	Gly
55	Tyr	Pro	o Gli			ı Ası	n Pro	o Glu	ı Ala		u Gly	/ Phe	e Se	r Pro		ı Asp
				100	O				10	_					,	

			115					120					125			
5	Asp	Gly 130	Tyr	Ala	Arg	Gly	Ala 135	Gln	Gln	Leu	Ala	Ala 140	Ala	Ala	Gly	Ala
J	Gly 145	Ala	Gly	Ala	Ser	Leu 150	Gly	Gly	Ser	Gly	Glu 155	Glu	Met	Gly	Pro	Ala
10	Ala	Ala	Val	Val	Ser 165	Ala	Val	Ile	Ala	Ala 170	Ala	Ala	Ala	Gln	Ser 175	Gly
	Ala	Gly	Pro	His 180	Tyr	His	His	His	His 185	His	His	Ala	Ala	Gly 190	His	His
15	His	His	Pro 195	Thr	Ala	Gly	Ala	Pro 200	Gly	Ala	Ala	Gly	Ser 205	Ala	Ala	Ala
20	Ser	Ala 210	Gly	Gly	Ala	Gly	Gly 215	Ala	Gly	Gly	Gly	Gly 220	Pro	Ala	Ser	Val
	Gly 225	Gly	Gly	Gly	Gly	Gly 230	Gly	Gly	Gly	Gly	Gly 235	Gly	Gly	Gly	Ala	Ala 240
25	Gly	Ala	Leu	His	Pro 245	His	His	Ala	Ala	Gly 250	Gly	Leu	His	Phe	Asp 255	Asp
	Arg	Phe	Ser	Asp 260	Glu	Gln	Leu	Val	Thr 265	Met	Ser	Val	Arg	Asp 270	Trp	Asr
30	Arg	Gln	Leu 275	Arg	Gly	Val	Ser	Lys 280	Glu	Glu	Val	Ile	Arg 285	Leu	Lys	Glr
35	Lys	Arg 290	Arg	Thr	Leu	Lys	Asn 295	Arg	Gly	Tyr	Ala	Lys 300	Ser	Cys	Arg	Phe
	Lys 305	Arg	Val	Gln	Gln	Arg 310	His	Val	Leu	Glu	Ser 315	Glu	Lys	Asn	Gln	Let 320
40	Leu	Gln	Gln	Val	Asp 325	His	Leu	Lys	Gln	Glu 330	Ile	Ser	Arg	Leu	Val 335	Arg
	Glu	Arg	Asp	Ala 340	Tyr	Lys	Glu	Lys	Tyr 345	Glu	Lys	Leu	Val	Ser 350	Ser	GlΣ
45	Phe	Arg	Glu 355	Asn	Gly	Ser	Ser	Ser 360	Asp	Asn	Pro	Ser	Ser 365	Pro	Glu	Phe
50	Phe	Ile 370	Thr	Glu	Pro	Thr	Arg 375	Lys	Leu	Glu	Pro	Ser 380	Val	Gly	Tyr	Ala
	Thr		Trp	Lys	Pro	Gln 390	His	Arg	Val	Leu	Thr		Val	Phe	Thr	Ly: